



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/671,304 B
Source: ITL
Date Processed by STIC: 10-18-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer-Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/671,304B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was received in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO. X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO. X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.

8 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.

11 Use of <220> Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/671,304B

DATE: 10/18/2004

TIME: 14:16:29

Input Set : A:\18528.643.SeqList.txt

Output Set: N:\CRF4\10182004\J671304B.raw

3 <110> APPLICANT: Gedulin, Bronislava
 4 Young, Andrew A.
 6 <120> TITLE OF INVENTION: Treatment of Pancreatitis with Amylin
 8 <130> FILE REFERENCE: 18528.643
 10 <140> CURRENT APPLICATION NUMBER: 10/671,304B
 C--> 11 <141> **CURRENT FILING DATE: 2003-09-24**
 13 <150> PRIOR APPLICATION NUMBER: 60/419,440
 14 <151> PRIOR FILING DATE: 2002-10-18
 16 <160> NUMBER OF SEQ ID NOS: 2
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 37
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Human
 25 <400> SEQUENCE: 1
 27 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
 28 1 5 10 15
 31 Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val
 32 20 25 30
 35 Gly Ser Asn Thr Tyr
 36 35
 39 <210> SEQ ID NO: 2
 40 <211> LENGTH: 37
 41 <212> TYPE: PRT
 42 <213> ORGANISM: Artificial Sequence
 44 <220> FEATURE:
 45 <223> OTHER INFORMATION: none
 47 <220> FEATURE:
 48 <221> NAME/KEY: MISC_FEATURE
 49 <222> LOCATION: (1)..(1)
 50 <223> OTHER INFORMATION: X is Lys, Ala, Ser or hydrogen
 53 <220> FEATURE:
 54 <221> NAME/KEY: MISC_FEATURE
 55 <222> LOCATION: (2)..(2)
 56 <223> OTHER INFORMATION: X at position 2 and X at position 7 are independently
 selected am
 57 ino acid residues having side chains which are chemically bonded
 58 to each other to form an intramolecular linkage
 61 <220> FEATURE:
 62 <221> NAME/KEY: MISC_FEATURE
 63 <222> LOCATION: (7)..(7)
 64 <223> OTHER INFORMATION: X at position 2 and X at position 7 are independently
 selected am
 65 ino acid residues having side chains which are chemically bonded

Does Not Comply
 Corrected Diskette Needed
 (P3.1)

Pls explain source of genetic material.
 Invalid Response
 See item # 11 on error Summary Sheet.

66 to each other to form an intramolecular linkage

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Input Set : A:\18528.643.SeqList.txt

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69 <220> FEATURE:
70 <221> NAME/KEY: MISC_FEATURE
71 <222> LOCATION: (13)..(13)
72 <223> OTHER INFORMATION: X is Ala, Ser or Thr
75 <220> FEATURE:
76 <221> NAME/KEY: MISC_FEATURE
77 <222> LOCATION: (17)..(17)
78 <223> OTHER INFORMATION: X is Val, Leu or Ile
81 <220> FEATURE:
82 <221> NAME/KEY: MISC_FEATURE
83 <222> LOCATION: (18)..(18)
84 <223> OTHER INFORMATION: X is His or Arg
87 <220> FEATURE:
88 <221> NAME/KEY: MISC_FEATURE
89 <222> LOCATION: (19)..(19)
90 <223> OTHER INFORMATION: X is Ser or Thr
93 <220> FEATURE:
94 <221> NAME/KEY: MISC_FEATURE
95 <222> LOCATION: (20)..(20)
96 <223> OTHER INFORMATION: X is Ser, Thr, Gln or Asn
99 <220> FEATURE:
100 <221> NAME/KEY: MISC_FEATURE
101 <222> LOCATION: (21)..(21)
102 <223> OTHER INFORMATION: X is Asn, Gln or His
105 <220> FEATURE:
106 <221> NAME/KEY: MISC_FEATURE
107 <222> LOCATION: (23)..(23)
108 <223> OTHER INFORMATION: X is Phe, Leu or Tyr
111 <220> FEATURE:
112 <221> NAME/KEY: MISC_FEATURE
113 <222> LOCATION: (25)..(25)
114 <223> OTHER INFORMATION: X is Ala or Pro
117 <220> FEATURE:
118 <221> NAME/KEY: MISC_FEATURE
119 <222> LOCATION: (26)..(26)
120 <223> OTHER INFORMATION: X is Ile, Val, Ala or Leu
123 <220> FEATURE:
124 <221> NAME/KEY: MISC_FEATURE
125 <222> LOCATION: (28)..(28)
126 <223> OTHER INFORMATION: X is Ser, Pro, Leu, Ile or Thr
129 <220> FEATURE:
130 <221> NAME/KEY: MISC_FEATURE
131 <222> LOCATION: (29)..(29)
132 <223> OTHER INFORMATION: X is Ser, Pro or Thr
135 <220> FEATURE:
136 <221> NAME/KEY: MISC_FEATURE
137 <222> LOCATION: (31)..(31)
138 <223> OTHER INFORMATION: X is Asn, Asp, or Gln
141 <400> SEQUENCE: 2

RAW SEQUENCE LISTING

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Input Set : A:\18528.643.SeqList.txt

Output Set: N:\CRF4\10182004\J671304B.raw

W--> 143 Xaa Xaa Asn Thr Ala Thr Xaa Ala Thr Gln Arg Leu Xaa Asn Phe Leu
144 1 5 10 15
147 Xaa Xaa Xaa Xaa Xaa Asn Xaa Gly Xaa Xaa Leu Xaa Xaa Thr Xaa Val
148 20 25 30
151 Gly Ser Asn Thr Tyr
152 35

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 10/18/2004

PATENT APPLICATION: US/10/671,304B

TIME: 14:16:30

Input Set : A:\18528.643.SeqList.txt

Output Set: N:\CRF4\10182004\J671304B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1,2,7,13,17,18,19,20,21,23,25,26,28,29,31

VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/671,304B**

DATE: 10/18/2004

TIME: 14:16:30

Input Set : **A:\18528.643.SeqList.txt**

Output Set: **N:\CRF4\10182004\J671304B.raw**

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
M:341 Repeated in SeqNo=2